

#15

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/466,343BDATE: 12/17/96
TIME: 11:03:58

INPUT SET: S14433.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: LI, Yi

(ii) TITLE OF INVENTION: Human G-Protein Chemokine
Receptor HSATU68

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein

(B) STREET: 6 Becker Farm Road

(C) CITY: Roseland

(D) STATE: NJ

(E) COUNTRY: USA

(F) ZIP: 07068-1739

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WordPerfect 5.1, Dos Text File

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/466,343

(B) FILING DATE: 6 JUN 1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MULLINS, J.G.

(B) REGISTRATION NUMBER: 33,073

(C) REFERENCE/DOCKET NUMBER: 325800-449

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700

(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1414 BASE PAIRS

(B) TYPE: NUCLEIC ACID

Does Not Comply
Corrected Diskette Needed

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47 (C) STRANDEDNESS: SINGLE
 48 (D) TOPOLOGY: LINEAR

49
 50 (ii) MOLECULE TYPE: cDNA

51
 52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 53

54 GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60
 55 GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120
 56
 57 TTAATTCAAT GTAGACATCT ATGTAGGCAA TAAAAACCT ATTGATGTAT AAAACAGTTT 180
 58
 59 GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTATTA 240
 60
 61 TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
 62 *see note above* Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
 63 1 5 10
 64 ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
 65 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
 66 15 20
 67 ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
 68 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
 69
 70 GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
 71 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
 72
 73 AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
 74 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
 75
 76 GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
 77 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
 78
 79 GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
 80 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr
 81
 82 TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
 83 Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr
 84
 85 ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675
 86 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
 87
 88 AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723
 89 Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
 90
 91 GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771
 92 Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
 93
 94 GAA GGT CTT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT 819
 95 Glu Gly Leu His Tyr Thr cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
 96
 97 CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867
 98 Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
 99

*please note:
 per 1.822(m) of sequence
 Rules, please number
 amino acids. (This even applies
 in
 a
 nuclear
 acid
 sequence)*

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100  GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA      915
101  Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
102
103  ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG      963
104  Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
105
106  CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC      1011
107  Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
108
109  AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT      1059
110  Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
111
112  AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG      1107
113  Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
114
115  ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT      1155
116  Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
117
118  GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC      1203
119  Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
120
121  ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT      1251
122  Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala
123
124  CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA      1299
125  Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu
126
127  ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG      1354
128  Ile Ser Val Gly Leu
129
130  TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT 1414
131
132
133  (2) INFORMATION FOR SEQ ID NO:2:
134      (i) SEQUENCE CHARACTERISTICS:
135          (A) LENGTH: 352 AMINO ACIDS
136          (B) TYPE: AMINO ACID
137          (C) STRANDEDNESS:
138          (D) TOPOLOGY: LINEAR
139
140      (ii) MOLECULE TYPE: PROTEIN
141
142      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
143
144  Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr
145              5                      10                      15
146
147  Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala
148              20                      25                      30
149
150  Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe
151              35                      40                      45
152

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153	Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg	
154		50 55 60
155		
156	Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser	
157		65 70 75
158		
159	Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala	
160		80 85 90
161		
162	Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly	
163		95 100 105
164		
165	Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln	
166		110 115 120
167		
168	Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe	
169		125 130 135
170		
171	Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val	
172		140 145 150
173		
174	Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile	
175		155 160 165
176		
177	Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr cys Ser Ser	
178		170 175 180
179		
180	His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr	
181		185 190 195
182		
183	Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met	
184		200 205 210
185		
186	Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg	
187		215 220 225
188		
189	Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile	
190		230 235 240
191		
192	Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu	
193		245 250 255
194		
195	Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser	
196		260 265 270
197		
198	Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu	
199		275 280 285
200		
201	Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val	
202		290 295 300
203		
204	Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His	
205		305 310 315

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206
207 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu
208 320 325 330
209
210 Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
211 335 340 345
212
213 Gln Glu Ile Ser Val Gly Leu
214 350
215
216
217

218 (2) INFORMATION FOR SEQ ID NO:3:
219

220 (i) SEQUENCE CHARACTERISTICS:
221 (A) LENGTH: 30 BASE PAIRS
222 (B) TYPE: NUCLEIC ACID
223 (C) STRANDEDNESS: SINGLE
224 (D) TOPOLOGY: LINEAR
225

226 (ii) MOLECULE TYPE: Oligonucleotide
227228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
229230 CGGAATTCCT CCATGGATTA TCAAGTGTCA
23130
232
233
234235 (2) INFORMATION FOR SEQ ID NO:4:
236

237 (i) SEQUENCE CHARACTERISTICS:
238 (A) LENGTH: 29 BASE PAIRS
239 (B) TYPE: NUCLEIC ACID
240 (C) STRANDEDNESS: SINGLE
241 (D) TOPOLOGY: LINEAR
242

243 (ii) MOLECULE TYPE: Oligonucleotide
244245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
246247 CGGAAGCTTC GTCACAAGCC CACAGATAT
24829
249249 (2) INFORMATION FOR SEQ ID NO:5:
250

251 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 34 BASE PAIRS
253 (B) TYPE: NUCLEIC ACID
254 (C) STRANDEDNESS: SINGLE
255 (D) TOPOLOGY: LINEAR
256

257 (ii) MOLECULE TYPE: Oligonucleotide
258